Amendment to the Claims

This listing of claims will replace all prior versions and listings of claims in the above-referenced application.

1. (currently amended) A transgenic *C. elegans* nematode, the cells of which contain a transgene comprising a regulatory element of the *C. elegans vap-1* [[a]] gene ~~that encodes a nematode secretory product or a homolog thereof~~ operably linked to a DNA sequence encoding a detectable marker, wherein the detectable marker is expressed in a *C. elegans* ~~pharyngeal gland cell or~~ amphid sheath cell.

2. (currently amended) The transgenic nematode of claim 1, wherein the transgene further comprises at least a portion of the coding sequence of the *C. elegans vap-1* gene.

3. (currently amended) The transgenic nematode of claim 2, wherein the transgene further comprises at least a portion of an intron from the *C. elegans vap-1* gene.

4. (currently amended) The transgenic nematode of claim 2, wherein the transgene further comprises at least a portion of the 3' untranslated region from the *C. elegans vap-1* gene.

5. (currently amended) The transgenic nematode of claim 2, wherein the coding sequence of the *C. elegans vap-1* gene is in frame with the sequence encoding the detectable marker.

6. (original) The transgenic nematode of claim 1, wherein the transgene is contained in a chromosome.

7. (original) The transgenic nematode of claim 1, wherein the transgene is extrachromosomal.

8. (original) The transgenic nematode of claim 5, wherein the transgene comprises an integrated array comprising a second regulatory element operably linked to a second copy of a DNA sequence encoding the detectable marker.

9. (original) The transgenic nematode of claim 8, wherein the second regulatory element directs expression of the detectable marker in a substantially different population of cells to that in which the first regulatory element directs expression of the detectable marker.

10. (canceled)

11. (original) The transgenic nematode of claim 1, wherein the detectable marker is selected from the list consisting of: a fluorescent polypeptide, a chemiluminescent polypeptide, an epitope tag, and an enzyme.

12. (previously presented) The transgenic nematode of claim 1, wherein the detectable marker is selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag.

13. (previously presented) The transgenic nematode of claim 1, wherein the detectable marker comprises a variant of a marker selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag, wherein the variant is detectable using the same detection means by which the marker of which it is a variant is detectable.

14-24. (canceled)

25. (currently amended) The transgenic nematode of claim 1, wherein the regulatory element is a 5' regulatory region comprising between 1 nucleotide and 10 kB of sequence extending in a 5' direction from the start codon of the *C. elegans vap-1* gene.

26-45. (canceled)

46. (previously presented) A method of generating a nematode comprising steps of:

(a) selecting a parasitic nematode secretory protein;

(b) identifying a *C. elegans* homolog of the protein selected in step (a);

(c) identifying a nucleic acid sequence comprising a regulatory region of a *C. elegans* gene encoding the *C. elegans* homolog identified in step (b); and

(d) generating a transgenic *C. elegans* nematode, wherein cells of the transgenic nematode comprise a nucleic acid sequence including the identified regulatory region operably linked to a nucleic acid sequence encoding a detectable marker, wherein the detectable marker is expressed in a pharyngeal gland cell or amphid sheath cell.

47. (currently amended) The method of claim 46, wherein the parasitic nematode is a member of an order selected from the group consisting of the *Strongylida, Rhabditida, Ascaridida, Spirurida, Oxyurida, Enoplida, Tylenchida,* or *Dorylaimida* nematode orders ~~a *Tylenchid* nematode~~.

48. (original) The method of claim 46, wherein the regulatory region comprises a promoter of the *C. elegans* homolog identified in step (b).

49. (original) The method of claim 46, wherein the nucleic acid sequence of step (d) includes at least a portion of the coding sequence of a gene encoding the *C. elegans* homolog of part (c).

50. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes a signal sequence.

51. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes at least a portion of an intron from a gene encoding the *C. elegans* homolog of part (c).

52. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes at least a portion of the 3' untranslated region from a gene encoding the *C. elegans* homolog of part (c).

53. (original) The method of claim 46, wherein the regulatory region is sufficient to direct expression of the nucleic acid of step (d).

54-105. (canceled)

106. (currently amended) A method of expressing a ~~first~~ polynucleotide in a *C. elegans* nematode comprising the step of:

generating a transgenic *C. elegans* nematode, cells of which comprise a transgene comprising a *C. elegans* *vap-1* regulatory region operably linked to the ~~first~~ polynucleotide; and

maintaining the *C. elegans* nematode so that expression of the ~~first~~ polynucleotide occurs in an amphid sheath cell.

107. (previously presented) The method of claim 106, wherein the polynucleotide encodes a polypeptide.

108. (previously presented) The method of claim 106, wherein the transgene comprises between 1 nucleotide and 10kB of sequence extending in a 5' direction from the start codon of the *C. elegans* *vap-1* gene.

109. (currently amended) The method of claim 106, wherein the generating step comprises injecting a polynucleotide into a *C. elegans* nematode, wherein the polynucleotide comprises a *C. elegans* *vap-1* regulatory region operably linked to the polynucleotide.

110-130. (canceled)

131. (previously presented) The method of claim 106, wherein the polynucleotide encodes a detectable marker.

132. (previously presented) The method of claim 131, wherein the detectable marker is selected from the list consisting of: a fluorescent polypeptide, a chemiluminescent polypeptide, an epitope tag, and an enzyme.

133. (previously presented) The method of claim 131, wherein the detectable marker is selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl

transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag.

134. (previously presented) The method of claim 131, wherein the detectable marker comprises a variant of a marker selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag, wherein the variant is detectable using the same detection means by which the marker of which it is a variant is detectable.

135. (previously presented) The method of claim 131, wherein the detectable marker is alkaline phosphatase.

136. (currently amended) The method of claim 106, wherein the transgene further comprises at least a portion of the coding sequence of the *C. elegans vap-1* gene, at least a portion of an intron of the *C. elegans vap-1* gene, at least a portion of the 3' untranslated region of the *C. elegans vap-1* gene, or any combination of the foregoing.

137 – 142. (canceled)

143. (new) The method of claim 46, wherein the parasitic nematode is a member of a genus selected from the list consisting of the *Haemonchus, Oestertagia, Trichostrongylus, Cooperia, Dictyocaulus, Strongylus, Oesophagostomum, Syngamus, Nematodirus, Heligmosomoides, Nippostrongylus, Metastrongylus, Angiostrongylus, Ancylostoma, Necator, Uncinaria, Bunostomum, Strongyloides, Steinernema, Ascaris, Parascaris, Toxocara, Toxascaris, Baylisascaris, Anisakis, Pseudoterranova, Heterakis, Wuchereria, Brugia, Onchocerca, Dirofilaria, Loa, Thelazia, Dracunculus, Gnathostoma, Enterobius, Oxyuris, Syphacia, Trichinella, Trichuris, Capillaria, Globodera, Heterodera, Meloidogyne, Anguina, Ditylenchus, Hirschmanniella, Naccobus, Pratylenchus, Radopholus, Criconema, Tylenchulus, Paratylenchus, Aphelenchus, Bursaphelenchus, Longidorus, Xiphinema, Trichodorus,* and *Paratrichodorus* nematode genera.